



BLASTP 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1086373128-6257-149750166997.BLASTQ4

Query=

(91 letters)

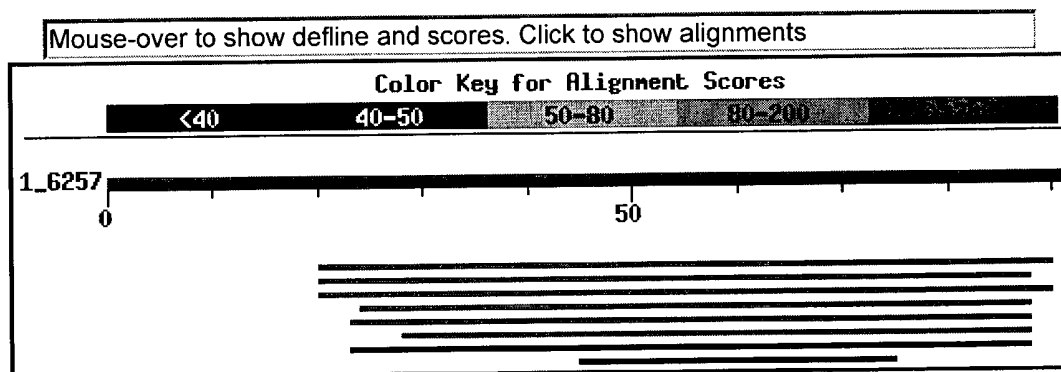
Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples
1,846,720 sequences; 611,532,004 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 8 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Score E
(bits) Value

gi 27479893 ref XP_211736.1	hypothetical protein XP_211736...	140	8e-33	L
gi 28204858 gb AAH46522.1	Unknown (protein for IMAGE:50608...	137	7e-32	
gi 37182157 gb AAQ88881.1	RGPG542 [Homo sapiens]	130	1e-29	
gi 41148699 ref XP_372041.1	similar to RPLK9433 [Homo sapi...	104	6e-22	L
gi 47225703 emb CAG08046.1	unnamed protein product [Tetrao...	97	7e-20	
gi 47214434 emb CAF95769.1	unnamed protein product [Tetrao...	84	1e-15	
gi 47224583 emb CAG03567.1	unnamed protein product [Tetrao...	38	0.071	
gi 16754844 emb CAD10675.2	Mig1 protein [Debaryomyces occi...	31	6.4	

Alignments

☐ Get selected sequences☐ Select all☐ Deselect all

☐ >gi|27479893|ref|XP_211736.1| ☒ hypothetical protein XP_211736 [Homo sapiens]
Length = 152

Score = 140 bits (352), Expect = 8e-33
Identities = 71/71 (100%), Positives = 71/71 (100%)

Query: 21 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 80
EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR
Sbjct: 81 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 140

Query: 81 LAVSPVCMEDK 91
LAVSPVCMEDK
Sbjct: 141 LAVSPVCMEDK 151

☐ >gi|28204858|gb|AAH46522.1| Unknown (protein for IMAGE:5060814) [Mus musculus]
Length = 298

Score = 137 bits (344), Expect = 7e-32
Identities = 68/69 (98%), Positives = 69/69 (100%)

Query: 21 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 80
EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR
Sbjct: 229 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 288

Query: 81 LAVSPVCME 89
LAVSP+CME
Sbjct: 289 LAVSPMCME 297

☐ >gi|37182157|gb|AAQ88881.1| RGP542 [Homo sapiens]
Length = 91

Score = 130 bits (326), Expect = 1e-29
Identities = 71/71 (100%), Positives = 71/71 (100%)

Query: 21 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 80
EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR
Sbjct: 21 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 80

Query: 81 LAVSPVCMEDK 91
LAVSPVCMEDK
Sbjct: 81 LAVSPVCMEDK 91

☐ >gi|41148699|ref|XP_372041.1| ☒ similar to RPLK9433 [Homo sapiens]
gi|46409458|ref|NP_997296.1| ☒ RPLK9433 [Homo sapiens]

gi|37181538|gb|AAQ88580.1| **L** RPLK9433 [Homo sapiens]
Length = 129

Score = 104 bits (259), Expect = 6e-22
Identities = 49/65 (75%), Positives = 58/65 (89%)

Query: 25 EIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRHLYHNTRDCTIPAYYKRCARLLTRLAVS 84
EI PRD +KDKF+KH TGP+ FSP+CSKHFRHLY+NTR+C+ PAYYKRCARLLTRLAVS
Sbjct: 64 EIFPRDSNLKDKFIKHFTGPVTFSPKCSKHFRHLYNTRCSTPAYYKRCARLLTRLAVS 123
Query: 85 PVCME 89
P+C +
Sbjct: 124 PLCSQ 128

gi|47225703|emb|CAG08046.1| unnamed protein product [Tetraodon nigroviridis]
Length = 157

Score = 97.4 bits (241), Expect = 7e-20
Identities = 47/67 (70%), Positives = 56/67 (83%), Gaps = 1/67 (1%)

Query: 24 VEIVPRDLRMKDKFLKHLT-GPLYFSPKCSKHFRHLYHNTRDCTIPAYYKRCARLLTRLA 82
+EI PRDL MK KF++H T GP+ FS +C FHRHLYHNTRDC+ PAYYKRCARLLTRLA
Sbjct: 90 IEIFPRDLNMKGKFIQHFTAGPVKFSSECRIQFHRHLYHNTRDCSRPAYYKRCARLLTRLA 149
Query: 83 VSPVCME 89
+SP+CM+
Sbjct: 150 MSPLCMQ 156

gi|47214434|emb|CAF95769.1| unnamed protein product [Tetraodon nigroviridis]
Length = 61

Score = 83.6 bits (205), Expect = 1e-15
Identities = 44/61 (72%), Positives = 52/61 (85%)

Query: 29 RDLRMKDKFLKHLTGPLYFSPKCSKHFRHLYHNTRDCTIPAYYKRCARLLTRLAVSPVCM 88
RD R K+KF++HLTGPLY + KC +HFH+LYH TRDCT+PA+YKRCARLLTRLA SP C
Sbjct: 1 RDP RHKEKFIRHLTGPLYVNKKCRRHFHKLYHTTRDCTLP AFYKRCARLLTRLANS PQCS 60
Query: 89 E 89
E
Sbjct: 61 E 61

gi|47224583|emb|CAG03567.1| unnamed protein product [Tetraodon nigroviridis]
Length = 137

Score = 37.7 bits (86), Expect = 0.071
Identities = 27/66 (40%), Positives = 30/66 (45%), Gaps = 27/66 (40%)

Query: 24 VEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRHLYHNTRDCTIPAYYKRCARLLTRLAV 83
V I P DL+ KDKF+K LT +KRCARLL RLAV
Sbjct: 98 VGISPIDLKKDKFIKILT-----FKRCARLLIRLAV 130
Query: 84 SPVCME 89

SP C E
Sbjct: 131 SPQCTE 136

☐ >gi|16754844|emb|CAD10675.2| Mig1 protein [Debaryomyces occidentalis]
Length = 458

Score = 31.2 bits (69), Expect = 6.4
Identities = 16/42 (38%), Positives = 19/42 (45%), Gaps = 11/42 (26%)

Query: 46 YFSPKCSKHFFHRLYHNTR-----DCTIPAYYKRCAR 76
Y P C K FHRL H TR CT P +K+ +R
Sbjct: 24 YKCPMCGKAFHRLEHQTRHIRTHTGEKPHSCTFPGCFKKFSR 65

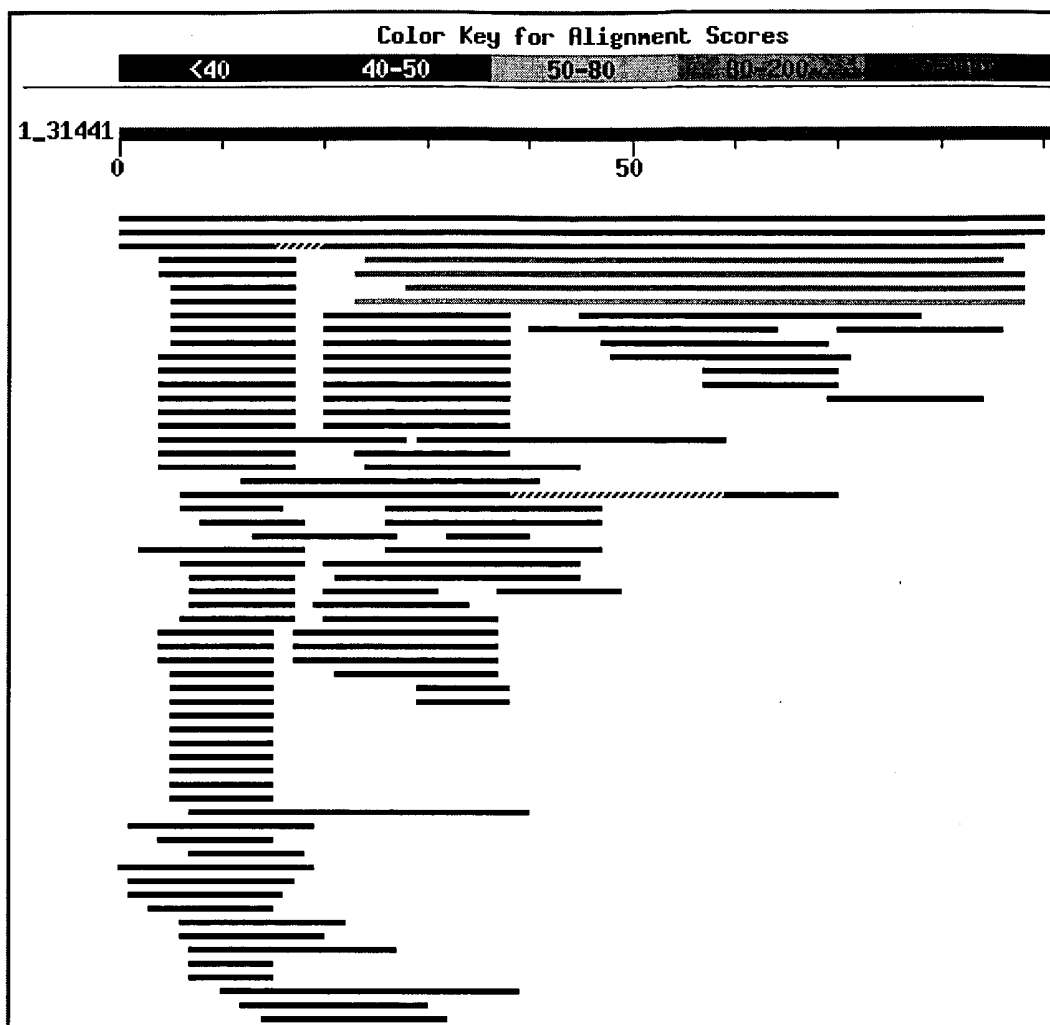
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
Posted date: Jun 2, 2004 2:29 AM
Number of letters in database: 611,532,004
Number of sequences in database: 1,846,720

Lambda K H
0.330 0.141 0.457

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 21,720,782
Number of Sequences: 1846720
Number of extensions: 704886
Number of successful extensions: 1600
Number of sequences better than 10.0: 3
Number of HSP's better than 10.0 without gapping: 3
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 1596
Number of HSP's gapped (non-prelim): 3
length of query: 91
length of database: 611,532,004
effective HSP length: 61
effective length of query: 30
effective length of database: 498,882,084
effective search space: 14966462520
effective search space used: 14966462520
T: 11
A: 40
X1: 15 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.8 bits)

S2: 68 (30.8 bits)



Sequences producing significant alignments:

	Score (bits)	E Value
gi 37182157 gb AAQ88881.1 RGPG542 [Homo sapiens]	302	3e-81
gi 27479893 ref XP_211736.1 hypothetical protein XP 211736...	261	5e-69
gi 28204858 gb AAH46522.1 Unknown (protein for IMAGE:50608...	230	1e-59
gi 41148699 ref XP_372041.1 similar to RPLK9433 [Homo sapi...	148	6e-35
gi 47225703 emb CAG08046.1 unnamed protein product [Tetrao...	136	2e-31
gi 47214434 emb CAF95769.1 unnamed protein product [Tetrao...	127	1e-28
gi 47224583 emb CAG03567.1 unnamed protein product [Tetrao...	57	2e-07
gi 6456546 gb AAF09175.1 UDP-glucuronosyltransferase 1A1 [...	37	0.23
gi 6456548 gb AAF09176.1 UDP-glucuronosyltransferase 1A1 [...	37	0.23
gi 31235852 ref XP_319311.1 ENSANGP00000022605 [Anopheles ...	35	0.75
gi 31235881 ref XP_319315.1 ENSANGP00000024583 [Anopheles ...	35	0.75
gi 31235868 ref XP_319313.1 ENSANGP00000023782 [Anopheles ...	35	0.75
gi 31235885 ref XP_319316.1 ENSANGP00000023510 [Anopheles ...	35	0.75
gi 31235859 ref XP_319312.1 ENSANGP00000025304 [Anopheles ...	35	0.75
gi 31235848 ref XP_319310.1 ENSANGP00000024621 [Anopheles ...	35	0.75
gi 31235836 ref XP_319308.1 ENSANGP00000012555 [Anopheles ...	35	0.75
gi 31235874 ref XP_319314.1 ENSANGP00000022367 [Anopheles ...	35	0.75
gi 31235842 ref XP_319309.1 ENSANGP00000024129 [Anopheles ...	35	0.75
gi 6456554 gb AAF09179.1 UDP-glucuronosyltransferase 1A1 [...	35	1.4

Clark, et al

gi 13641265 gb AAK31597.1 	UDP-glucuronosyltransferase UGT1...	35	1.4	
gi 6537144 gb AAF15549.1 	UDP-glucuronosyltransferase UGT1A...	35	1.4	
gi 13936939 gb AAK49991.1 	UDP-glucuronosyltransferase UGT1...	35	1.4	
gi 6456556 gb AAF09180.1 	UDP-glucuronosyltransferase 1A1 [...]	35	1.4	
gi 39998404 ref NP_954355.1 	major facilitator family trans...	33	3.3	
gi 13569709 gb AAK31204.1 	bilirubin UDP-glucuronosyltrasfer...	32	5.9	
gi 8850236 ref NP_000454.1 	UDP glycosyltransferase 1 famil...	32	5.9	L
gi 45199011 ref NP_986040.1 	AFR493Cp [Eremothecium gossypi...	32	5.9	
gi 3059177 dbj BAA25600.1 	bilirubin UDP-glucuronosyltransf...	32	5.9	
gi 6456550 gb AAF09177.1 	UDP-glucuronosyltransferase 1A1 [...]	32	5.9	
gi 38106605 gb EAA52893.1 	hypothetical protein MG06021.4 [...]	32	5.9	
gi 6010650 gb AAF01205.1 	bilirubin UDP-glucuronosyltransfe...	32	5.9	
gi 340132 gb AAA61248.1 	bilirubin UDP-glucuronosyltransferase	32	5.9	
gi 12002135 gb AAG43197.1 	UDP-glucuronosyltransferase [Hom...	32	5.9	
gi 6456542 gb AAF09173.1 	UDP-glucuronosyltransferase 1A1 [...]	32	5.9	
gi 15616196 ref NP_244501.1 	transcriptional regulator (Ara...	32	7.9	
gi 179419 gb AAA51822.1 	beta-galactosidase precursor (EC 3...	32	11	L
gi 39936770 ref NP_949046.1 	Globin-like protein [Rhodopseu...	32	11	
gi 17367360 sp Q63376 NX2B RAT	Neurexin 2-beta precursor (N...	32	11	L
gi 38099400 gb EAA46751.1 	hypothetical protein MG10445.4 [...]	32	11	
gi 23063144 ref ZP_00087886.1 	hypothetical protein [Pseudo...	32	11	
gi 19745439 ref NP_606575.1 	putative ABC transporter (perm...	31	14	
gi 15674485 ref NP_268659.1 	putative ABC transporter (perm...	31	14	
gi 21909771 ref NP_664039.1 	putative ABC transporter (perm...	31	14	
gi 34328319 ref NP_083633.2 	RIKEN cDNA 2010005A06 [Mus mus...	31	14	L
gi 19115312 ref NP_594400.1 	hypothetical protein [Schizosa...	31	14	
gi 21673770 ref NP_661835.1 	FecCD transport family protein...	31	14	
gi 46362507 gb AAH66572.1 	LOC407707 protein [Danio rerio]	31	19	L
gi 40645690 dbj BAD06359.1 	putative integral membrane prot...	31	19	
gi 29830792 ref NP_825426.1 	putative integral membrane pro...	31	19	
gi 6456552 gb AAF09178.1 	UDP-glucuronosyltransferase 1A1 [...]	31	19	
gi 21222362 ref NP_628141.1 	possible integral membrane pro...	31	19	
gi 6806893 ref NP_000586.2 	lymphotoxin alpha precursor; ly...	30	26	L
gi 31880296 gb AAP51424.1 	lymphotoxin alpha precursor [Hom...	30	26	
gi 11875697 gb AAG40760.1 	urokinase plasminogen activator ...	30	26	
gi 37527109 ref NP_930453.1 	hypothetical protein [Photorha...	30	26	
gi 29247065 gb EAA38639.1 	GLP_59_9627_8422 [Giardia lambl...	30	26	
gi 31880292 gb AAP51422.1 	lymphotoxin alpha precursor [Hom...	30	26	
gi 31880318 gb AAP51435.1 	lymphotoxin alpha precursor [Hom...	30	26	
gi 31880294 gb AAP51423.1 	lymphotoxin alpha precursor [Hom...	30	26	
gi 339743 gb AAB59455.1 	tumor necrosis factor-beta	30	26	L
gi 31880290 gb AAP51421.1 	lymphotoxin alpha precursor [Hom...	30	26	
gi 46107834 ref XP_380976.1 	hypothetical protein FG00800.1...	30	26	
gi 356345 prf 1209233A	lymphotoxin	30	26	
gi 47117368 sp P61125 TNFB PANTR	Lymphotoxin-alpha precursore...	30	26	L
gi 2493675 sp Q28042 OGP BOVIN	OVIDUCT-SPECIFIC GLYCOPROTEI...	30	26	L
gi 11875701 gb AAG40762.1 	urokinase plasminogen activator ...	30	26	
gi 11875699 gb AAG40761.1 	urokinase plasminogen activator ...	30	26	
gi 219914 dbj BAA00064.1 	lymphotoxin [Homo sapiens] >gi 31...	30	26	L
gi 34499061 ref NP_903276.1 	conserved hypothetical protein...	30	34	
gi 7503491 pir T22238	hypothetical protein F45G2.6 - Caeno...	30	34	
gi 32565349 ref NP_499773.2 	TNF Receptor associated Factor...	30	34	L
gi 39586579 emb CAE73706.1 	Hypothetical protein CBG21219 [...]	30	34	
gi 11138413 gb AAG31358.1 	dipeptidyl carboxy peptidase 1 [...]	30	34	
gi 29249818 gb EAA41322.1 	GLP_163_36481_38211 [Giardia lam...	30	34	
gi 46366359 ref ZP_00228687.1 	COG1173: ABC-type dipeptide/...	30	34	

gi 19552109 ref NP_600111.1 	putative acetyltransferase [Co...	<u>29</u>	46	
gi 15612782 ref NP_241085.1 	L-lactate permease [Bacillus h...	<u>29</u>	46	
gi 16754844 emb CAD10675.2 	Mig1 protein [Debaryomyces occi...	<u>29</u>	46	
gi 26106036 dbj BAC41711.1 	poliovirus receptor [Cebus apella]	<u>29</u>	46	
gi 27381266 ref NP_772795.1 	ABC transporter ATP-binding pr...	<u>29</u>	46	
gi 6475037 dbj BAA87329.1 	sushi-repeat-containing protein ...	<u>29</u>	46	L
gi 41199583 ref XP_372161.1 	similar to CDNA sequence BC004...	<u>29</u>	46	L
gi 34558352 ref NP_908167.1 	hypothetical protein WS2068 [W...	<u>29</u>	46	
gi 46404433 gb AAS93256.1 	glutathione S-transferase [Oryza...	<u>29</u>	46	
gi 730164 sp Q02920 NO70 SOYBN	Early nodulin 70 >gi 486678 ...	<u>29</u>	46	
gi 34873536 ref XP_220919.2 	similar to mKIAA1136 protein [...]	<u>29</u>	46	L
gi 33599656 ref NP_887216.1 	putative exported protein [Bor...	<u>29</u>	46	
gi 47219318 emb CAG10947.1 	unnamed protein product [Tetrao...	<u>29</u>	46	
gi 23102087 ref ZP_00088614.1 	COG2998: ABC-type tungstate ...	<u>29</u>	46	
gi 37520203 ref NP_923580.1 	two-component hybrid sensor an...	<u>29</u>	46	
gi 16209647 gb AAL14384.1 	AT3g52500/F2206_120 [Arabidopsis...	<u>29</u>	46	
gi 23063253 ref ZP_00087995.1 	COG2822: Predicted periplasm...	<u>29</u>	46	
gi 4758686 ref NP_002323.1 	low density lipoprotein-related...	<u>29</u>	46	L
gi 45547567 ref ZP_00187613.1 	COG1038: Pyruvate carboxylas...	<u>29</u>	46	
gi 42408797 dbj BAD10058.1 	putative aminoacylase [Oryza sa...	<u>29</u>	46	
gi 21245005 ref NP_644587.1 	phytochrome-like protein [Xant...	<u>29</u>	46	
gi 845468 gb AAA67825.1 	precursor protein [Hepatitis C vir...	<u>29</u>	46	
gi 46130328 ref ZP_00165149.2 	COG0388: Predicted amidohydr...	<u>29</u>	46	
gi 21323650 dbj BAB98277.1 	Acetyltransferases, including N...	<u>29</u>	46	
gi 34540006 ref NP_904485.1 	hydrolase, carbon-nitrogen fam...	<u>29</u>	46	

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|37182157|gb|AAQ88881.1|](#) RGP542 [Homo sapiens]
Length = 91

Score = 302 bits (706), Expect = 3e-81
Identities = 91/91 (100%), Positives = 91/91 (100%)

Query: 1 MRGPGHPLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYH 60
MRGPGHPLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYH
Sbjct: 1 MRGPGHPLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYH 60

Query: 61 NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK 91
NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK
Sbjct: 61 NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK 91

☐ >[gi|27479893|ref|XP_211736.1|](#) **L** hypothetical protein XP_211736 [Homo sapiens]
Length = 152

Score = 261 bits (610), Expect = 5e-69
Identities = 91/151 (60%), Positives = 91/151 (60%), Gaps = 60/151 (39%)

Query: 1 MRGPGHPLL-----LG-----LL-----LV----- 15
MRGPGHPLL LG LL LV
Sbjct: 1 MRGPGHPLLGLLLVLGAAGRGRGGAEPREPADGQALLRLVVELVQELRKHHS AEHKGLQ 60

Score = 136 bits (315), Expect = 2e-31

Identities = 47/67 (70%), Positives = 56/67 (83%), Gaps = 1/67 (1%)

Query: 24 VEIVPRDLRMKDKFLKHLT-GPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTRLA 82
 +EI PRDL MK KF++H T GP+ FS +C FHRLYHNTRDC+ PAYYKRCARLLTRLA
 Sbjct: 90 IEIFPRDLNMKGKFIQHFTAGPVKFSSECRIQFHRLYHNTRDCSRPAYYKRCARLLTRLA 149

Query: 83 VSPVCME 89
 +SP+CM+
 Sbjct: 150 MSPLCMQ 156

☐ >gi|47214434|emb|CAF95769.1| unnamed protein product [Tetraodon nigroviridis]
 Length = 61

Score = 127 bits (294), Expect = 1e-28
 Identities = 44/61 (72%), Positives = 52/61 (85%)

Query: 29 RDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTRLAVSPVCM 88
 RD R K+KF++HLTGPLY + KC +HFH+LYH TRDCT+PA+YKRCARLLTRLA SP C
 Sbjct: 1 RDP RHKEKFIRHLTGPLYVNKKCRRHFKLYHTTRDCTLPAFYKRCARLLTRLANSPOCS 60

Query: 89 E 89
 E
 Sbjct: 61 E 61

☐ >gi|47224583|emb|CAG03567.1| unnamed protein product [Tetraodon nigroviridis]
 Length = 137

Score = 57.5 bits (128), Expect = 2e-07
 Identities = 28/66 (42%), Positives = 31/66 (46%), Gaps = 27/66 (40%)

Query: 24 VEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTRLAV 83
 V I P DL+ KDKF+K LT D +KRCARLL RLAV
 Sbjct: 98 VGISPIDLKKKDKFIKILT-----D-----FKRCARLLIRLAV 130

Query: 84 SPVCME 89
 SP C E
 Sbjct: 131 SPQCTE 136

☐ >gi|6456546|gb|AAF09175.1| UDP-glucuronosyltransferase 1A1 [Gorilla gorilla]
 Length = 25

Score = 37.1 bits (80), Expect = 0.23
 Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
 GHPL+LGLLL VLGP
 Sbjct: 8 GHPLVLGLLLCVLGP 22

☐ >gi|6456548|gb|AAF09176.1| UDP-glucuronosyltransferase 1A1 [Gorilla gorilla]
 Length = 29

Score = 37.1 bits (80), Expect = 0.23
Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
GHPL+LGLLL VLGP
Sbjct: 8 GHPLVLGLLLCVLGP 22

☐ >gi|31235852|ref|XP_319311.1| ENSANGP00000022605 [Anopheles gambiae]
gi|30174786|gb|EAA43612.1| ENSANGP00000022605 [Anopheles gambiae str. PEST]
Length = 1938

Score = 35.4 bits (76), Expect = 0.75
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 806 EQRVSLEIVQRNLR---KYLK 823

☐ >gi|31235881|ref|XP_319315.1| ENSANGP00000024583 [Anopheles gambiae]
gi|30174793|gb|EAA43618.1| ENSANGP00000024583 [Anopheles gambiae str. PEST]
Length = 1451

Score = 35.4 bits (76), Expect = 0.75
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 314 EQRVSLEIVQRNLR---KYLK 331

☐ >gi|31235868|ref|XP_319313.1| ENSANGP00000023782 [Anopheles gambiae]
gi|30174788|gb|EAA43614.1| ENSANGP00000023782 [Anopheles gambiae str. PEST]
Length = 1739

Score = 35.4 bits (76), Expect = 0.75
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 602 EQRVSLEIVQRNLR---KYLK 619

☐ >gi|31235885|ref|XP_319316.1| ENSANGP00000023510 [Anopheles gambiae]
gi|30174790|gb|EAA43616.1| ENSANGP00000023510 [Anopheles gambiae str. PEST]
Length = 1315

Score = 35.4 bits (76), Expect = 0.75
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 152 EQRVSLEIVQRNLR---KYLK 169

□>gi|31235859|ref|XP_319312.1| ENSANGP00000025304 [Anopheles gambiae]
gi|30174794|gb|EAA43619.1| ENSANGP00000025304 [Anopheles gambiae str. PEST]
Length = 1938

Score = 35.4 bits (76), Expect = 0.75
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 806 EQRVSLEIVQRNLR---KYLK 823

□>gi|31235848|ref|XP_319310.1| ENSANGP00000024621 [Anopheles gambiae]
gi|30174789|gb|EAA43615.1| ENSANGP00000024621 [Anopheles gambiae str. PEST]
Length = 1937

Score = 35.4 bits (76), Expect = 0.75
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 806 EQRVSLEIVQRNLR---KYLK 823

□>gi|31235836|ref|XP_319308.1| ENSANGP00000012555 [Anopheles gambiae]
gi|30174792|gb|EAA13871.2| ENSANGP00000012555 [Anopheles gambiae str. PEST]
Length = 1943

Score = 35.4 bits (76), Expect = 0.75
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 806 EQRVSLEIVQRNLR---KYLK 823

□>gi|31235874|ref|XP_319314.1| ENSANGP00000022367 [Anopheles gambiae]
gi|30174791|gb|EAA43617.1| ENSANGP00000022367 [Anopheles gambiae str. PEST]
Length = 1644

Score = 35.4 bits (76), Expect = 0.75
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 507 EQRVSLEIVQRNLR---KYLK 524

□>gi|31235842|ref|XP_319309.1| ENSANGP00000024129 [Anopheles gambiae]
gi|30174787|gb|EAA43613.1| ENSANGP00000024129 [Anopheles gambiae str. PEST]
Length = 1937

Score = 35.4 bits (76), Expect = 0.75
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 806 EQRVSLEIVQRNLR---KYLK 823

☐ >[gi|6456554|gb|AAF09179.1|](#) UDP-glucuronosyltransferase 1A1 [Papio cynocephalus]
Length = 28

Score = 34.6 bits (74), Expect = 1.4
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLLL-VLGP 18
HPL+LGLLLL VLGP
Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >[gi|13641265|gb|AAK31597.1|](#) UDP-glucuronosyltransferase UGT1A01 [Macaca mulatta]
Length = 533

Score = 34.6 bits (74), Expect = 1.4
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLLL-VLGP 18
HPL+LGLLLL VLGP
Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >[gi|6537144|gb|AAF15549.1|](#) UDP-glucuronosyltransferase UGT1A01 [Macaca fascicula]
Length = 533

Score = 34.6 bits (74), Expect = 1.4
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLLL-VLGP 18
HPL+LGLLLL VLGP
Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >[gi|13936939|gb|AAK49991.1|](#) UDP-glucuronosyltransferase UGT1A01 [Macaca mulatta]
Length = 533

Score = 34.6 bits (74), Expect = 1.4
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLLL-VLGP 18
HPL+LGLLLL VLGP
Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >[gi|6456556|gb|AAF09180.1|](#) UDP-glucuronosyltransferase 1A1 [Colobus guereza]

Length = 28

Score = 34.6 bits (74), Expect = 1.4

Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLL-VLGP 18

HPL+LGLLL VLGP

Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >[gi|39998404|ref|NP_954355.1|](#) major facilitator family transporter [Geobacter su
[gi|39985351|gb|AAR36705.1|](#) major facilitator family transporter [Geobacter sulfur

Length = 414

Score = 33.3 bits (71), Expect = 3.3

Identities = 16/27 (59%), Positives = 17/27 (62%), Gaps = 7/27 (25%)

Query: 5 GHPLLLGLLLV--LGPSPEQRVEIVPR 29

G LLL LLLV LGP+ EQ VPR

Sbjct: 292 GQSLLLFLLLVLTLGPA-EQ----VPR 313

☐ >[gi|13569709|gb|AAK31204.1|](#) bilirubin UDP-glucuronosyltransferase 1-1 [Homo sapien

Length = 66

Score = 32.5 bits (69), Expect = 5.9

Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLLV-VLGP 18

G PL+LGLLL VLGP

Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|8850236|ref|NP_000454.1|](#) ☒ UDP glycosyltransferase 1 family, polypeptide A1
bilirubin UDP-glucuronosyltransferase isozyme 1 [Homo
sapiens]

[gi|136729|sp|P22309|UD11_HUMAN](#) ☒ UDP-glucuronosyltransferase 1-1 precursor, micro
(UDP-glucuronosyltransferase 1A1) (UDPGT) (UGT1*1)
(UGT1-01) (UGT1.1) (UGT-1A) (UGT1A) (Bilirubin specific
UDPGT isozyme 1) (HUG-BR1)

[gi|87534|pir||A39092](#) glucuronosyltransferase (EC 2.4.1.17) 1 precursor,
bilirubin-specific - human

[gi|184473|gb|AAA63195.1|](#) ☒ UDP-glucuronosyltransferase 1

[gi|6094671|gb|AAF03522.1|](#) ☒ UDP-glucuronosyltransferase 1 [Homo sapiens]

[gi|11118749|gb|AAG30424.1|](#) UDP glucuronosyltransferase 1A1 [Homo sapiens]

[gi|40849850|gb|AAR95637.1|](#) ☒ UDP glycosyltransferase 1 family polypeptide A1 [Hom

[gi|46518737|gb|AAS99732.1|](#) UDP glycosyltransferase 1 family, polypeptide A1 [Homo

[gi|742224|prf||2009308A](#) bilirubin UDP glucuronosyltransferase:ISOTYPE=1

Length = 533

Score = 32.5 bits (69), Expect = 5.9

Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLLV-VLGP 18

G PL+LGLLL VLGP

Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|45199011|ref|NP_986040.1|](#) AFR493Cp [Eremothecium gossypii]
[gi|44985086|gb|AAS53864.1|](#) AFR493Cp [Eremothecium gossypii]
 Length = 324

Score = 32.5 bits (69), Expect = 5.9
 Identities = 13/19 (68%), Positives = 13/19 (68%), Gaps = 6/19 (31%)

Query: 24 VEIVPRD---LRMKDKFLK 39
 VEIVPRD L M KFLK

Sbjct: 42 VEIVPRDSPHL-M--KFLK 57

☐ >[gi|3059177|dbj|BAA25600.1|](#) bilirubin UDP-glucuronosyltransferase 1 [Homo sapien]
 Length = 50

Score = 32.5 bits (69), Expect = 5.9
 Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
 G PL+LGLLL VLGP

Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|6456550|gb|AAF09177.1|](#) UDP-glucuronosyltransferase 1A1 [Pongo pygmaeus]
 Length = 27

Score = 32.5 bits (69), Expect = 5.9
 Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
 G PL+LGLLL VLGP

Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|38106605|gb|EAA52893.1|](#) hypothetical protein MG06021.4 [Magnaporthe grisea 7]
 Length = 419

Score = 32.5 bits (69), Expect = 5.9
 Identities = 18/33 (54%), Positives = 21/33 (63%), Gaps = 6/33 (18%)

Query: 13 LLVLGPSPEQRVEIVPR--DLRMKDKF-LKHLT 42
 LLVL PS QR IV R LR++D F L +LT

Sbjct: 170 LLVLSPS--QRAAIVARLSVLRIRD-FMLPNLT 199

☐ >[gi|6010650|gb|AAF01205.1|](#) bilirubin UDP-glucuronosyltransferase 1-1 [Homo sapie
[gi|13448829|gb|AAK27223.1|](#) bilirubin UDP-glucuronosyltransferase 1 [Homo sapiens]
 Length = 71

Score = 32.5 bits (69), Expect = 5.9

Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18

G PL+LGLLL VLGP

Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|340132|gb|AAA61248.1|](#) bilirubin UDP-glucuronosyltransferase
Length = 288

Score = 32.5 bits (69), Expect = 5.9

Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18

G PL+LGLLL VLGP

Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|12002135|gb|AAG43197.1|](#) UDP-glucuronosyltransferase [Homo sapiens]
Length = 294

Score = 32.5 bits (69), Expect = 5.9

Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18

G PL+LGLLL VLGP

Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|6456542|gb|AAF09173.1|](#) UDP-glucuronosyltransferase 1A1 [Pan paniscus]
[gi|6456544|gb|AAF09174.1|](#) UDP-glucuronosyltransferase 1A1 [Pan troglodytes]
Length = 29

Score = 32.5 bits (69), Expect = 5.9

Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18

G PL+LGLLL VLGP

Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|15616196|ref|NP_244501.1|](#) transcriptional regulator (AraC/XylS family) [Baci
C-125]
[gi|25350122|pir||B84104](#) transcription regulator (AraC/XylS family) BH3634 [import
Bacillus halodurans (strain C-125)
[gi|10176258|dbj|BAB07353.1|](#) transcriptional regulator (AraC/XylS family) [Bacillu
C-125]
Length = 300

Score = 32.0 bits (68), Expect = 7.9

Identities = 16/34 (47%), Positives = 18/34 (52%), Gaps = 8/34 (23%)

Query: 46 YFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLT 79

YF HFHRL+ T CT+ Y KR R LT

Sbjct: 35 YF-----HFHRLFKATVGCTMSEYIKR--RRLT 60